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		APPLICANT: Kim et al.					
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U.S. PATENT DOCUMENTS							
EXAMINER INITIAL		DOCUMENT NO.	DATE	NAME	CLASS	SUBCLASS	FILED DATE OFFICE APPROPRIATE
FOREIGN PATENT DOCUMENTS							
OTHER INFORMATION (Including Author, Title, Date, Pertinent Pages, Etc.)							
AM	A1 -	Bairoch. The Enzyme Database in 2000. <i>Nucl. Acids Res.</i> 28:304-305 (2000)					
	A2 -	Ben-Dor et al. Clustering gene expression patterns. <i>J. Comput. Biol.</i> 6(3/4): 281-297 (1999)					
	A3 -	Boguski et al. Biosequence Exegesis. <i>Science</i> 286(5439):453-455 (1999)					
	A4 -	Brown and Botstein. Exploring the new world of the genome with DNA microarrays. <i>Nat. Gene.</i> 21(1 Suppl):33-7 (1999)					
	A5 -	Chan et al. Microfabricated polymer devices for automated sample delivery of peptides for analysis by electrospray ionization tandem mass spectrometry. <i>Anal. Chem.</i> 71(20):4437-44 (1999)					
	A6 -	Cheng and Church. Biclustering of expression data. <i>ISMB</i> 93-103 (2000)					
	A7 -	Cherry et al. Genetic and physical maps of <i>Saccharomyces cerevisiae</i> . <i>Nature</i> 387(6632 Suppl.):67-73 (1997)					
	A8 -	Cherry et al. Saccharomyces Genome Database. http://genome-www.stanford.edu/Saccharomyces/ No pub. date					
AM	A9 -	Eisen et al. Cluster analysis and display of genome-wide expression patterns. <i>Proceedings of the Nat. Acad. Sci. USA</i> 95(25):14863-8 (1998)					
	A10 -	Forst and Schulten. Evolution of Metabolisms: A new method for the comparison of metabolic pathways using genomics information. <i>J. Comput. Biol.</i> 6:343-360 (1999)					
	A11 -	The Gene Ontology Consortium, Gene Ontology: tool for the unification of biology. <i>Nat. Gene.</i> 25: 25-29 (2000)					
	A12 -	Graves et al. A Graph-Theoretic Data Model for Genomic Mapping Databases. <i>Proceedings of the 28th Annual Hawaii International Conference on System Sciences</i> , 5:32-41 (1995)					

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	A14	Koch and Lengauer. Detection of distant structural similarities in a set of proteins using a fast graph-based method. <i>ISMB</i> , 5:167-78 (1997)
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	A16~	Ogata et al. Analysis of binary relations and hierarchies of enzymes in the metabolic pathways. <i>Biosys.</i> 47: 119-128 (1998)
	A17~	Patton. Making blind robots see: the synergy between fluorescent dyes and imaging devices in automated proteomics. <i>Biotech.</i> 28(5):944-8, 950-7 (2000)
	A18~	Robinson. Comparison of labeled trees with valency three. <i>J. Combin. Theor.</i> 11:105-119 (1971)
	A19	Rohlf. Consensus indices for comparing classifications. <i>Math. Biosci.</i> , 59:313-144 (1982)
	A20~	Samudrala and Moulton. A Graph-theoretic Algorithm for Comparative Modeling of Protein Structure. <i>J. Mol. Biol.</i> 279:287-302 (1998)
	A21~	Sharan and Shamir. CLICK: A clustering algorithm with applications to gene expression analysis. <i>ISMB</i> 2000, 307-316 (2000)
	A22~	Spellman et al. Comprehensive identification of cell cycle-regulated genes of the yeast <i>Saccharomyces cerevisiae</i> by microarray hybridization. <i>Mol Biol Cell</i> 9(12):3273-97 (1998)
	A23~	Steel and Penny. Distributions of tree comparison metrics. <i>Systematic Biology</i> 42:126-141 (1993)
	A24~	Tamayo et al. Interpreting patterns of gene expression with self-organizing maps: methods and application to hematopoietic differentiation. <i>Proc. Natl. Acad. Sci. USA</i> 96:2907-2912 (1999)
	A25~	Toba et al. The Gene Search System: A method for efficient detection and rapid molecular identification of genes in <i>Drosophila melanogaster</i> . <i>Gene</i> . 151:725-737 (1999)
	A26~	Uetz et al. A comprehensive analysis of protein-protein interactions in <i>Saccharomyces cerevisiae</i> . <i>Nature</i> 403(6770):623-7 (2000)
	A27~	Xenarios et al. DIP: the database of interacting proteins. <i>Nucl. Acids Res.</i> 28:289-91(2000)
EXAMINER: <i>Andin Marshall</i>		DATE CONSIDERED: <i>2-20-04</i>
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